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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/007,706

DATE: 07/02/2002
TIME: 13:57:13

Input Set : A:\A70040-1.ST25.txt
Output Set: N:\CRF3\07022002\J007706.raw

3 <110> APPLICANT: Penner, Reinhold
4 Fleig, Andrea
6 <120> TITLE OF INVENTION: METHODS OF SCREENING FOR LTRPC2 MODULATORS
8 <130> FILE REFERENCE: A-70040-1/RFT/NBC
10 <140> CURRENT APPLICATION NUMBER: US 10/007,706
11 <141> CURRENT FILING DATE: 2001-11-13
13 <150> PRIOR APPLICATION NUMBER: US 60/248,442
14 <151> PRIOR FILING DATE: 2000-11-13
16 <150> PRIOR APPLICATION NUMBER: US 60/254,528
17 <151> PRIOR FILING DATE: 2000-12-08
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1503
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
28 <400> SEQUENCE: 1
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31 1 5 10 15
34 Phe Glu Gly Leu Pro Arg Arg Val Thr Asp Leu Gly Met Val Ser Asn
35 20 25 30
38 Leu Arg Arg Ser Asn Ser Ser Leu Phe Lys Ser Trp Arg Leu Gln Cys
39 35 40 45
42 Pro Phe Gly Asn Asn Asp Lys Gln Glu Ser Leu Ser Ser Trp Ile Pro
43 50 55 60
46 Glu Asn Ile Lys Lys Glu Cys Val Tyr Phe Val Glu Ser Ser Lys
47 65 70 75 80
50 Leu Ser Asp Ala Gly Lys Val Val Cys Gln Cys Gly Tyr Thr His Glu
51 85 90 95
54 Gln His Leu Glu Glu Ala Thr Lys Pro His Thr Phe Gln Gly Thr Gln
55 100 105 110
58 Trp Asp Pro Lys Lys His Val Gln Glu Met Pro Thr Asp Ala Phe Gly
59 115 120 125
62 Asp Ile Val Phe Thr Gly Leu Ser Gln Lys Val Lys Lys Tyr Val Arg
63 130 135 140
66 Val Ser Gln Asp Thr Pro Ser Ser Val Ile Tyr His Leu Met Thr Gln
67 145 150 155 160
70 His Trp Gly Leu Asp Val Pro Asn Leu Leu Ile Ser Val Thr Gly Gly
71 165 170 175
74 Ala Lys Asn Phe Asn Met Lys Pro Arg Leu Lys Ser Ile Phe Arg Arg
75 180 185 190
78 Gly Leu Val Lys Val Ala Gln Thr Thr Gly Ala Trp Ile Ile Thr Gly
79 195 200 205

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82 Gly Ser His Thr Gly Val Met Lys Gln Val Gly Glu Ala Val Arg Asp
 83 210 215 220
 86 Phe Ser Leu Ser Ser Ser Tyr Lys Glu Gly Glu Leu Ile Thr Ile Gly
 87 225 230 235 240
 90 Val Ala Thr Trp Gly Thr Val His Arg Arg Glu Gly Leu Ile His Pro
 91 245 250 255
 94 Thr Gly Ser Phe Pro Ala Glu Tyr Ile Leu Asp Glu Asp Gly Gln Gly
 95 260 265 270
 98 Asn Leu Thr Cys Leu Asp Ser Asn His Ser His Phe Ile Leu Val Asp
 99 275 280 285
 102 Asp Gly Thr His Gly Gln Tyr Gly Val Glu Ile Pro Leu Arg Thr Arg
 103 290 295 300
 106 Leu Glu Lys Phe Ile Ser Glu Gln Thr Lys Glu Arg Gly Gly Val Ala
 107 305 310 315 320
 110 Ile Lys Ile Pro Ile Val Cys Val Val Leu Glu Gly Gly Pro Gly Thr
 111 325 330 335
 114 Leu His Thr Ile Asp Asn Ala Thr Thr Asn Gly Thr Pro Cys Val Val
 115 340 345 350
 118 Val Glu Gly Ser Gly Arg Val Ala Asp Val Ile Ala Gln Val Ala Asn
 119 355 360 365
 122 Leu Pro Val Ser Asp Ile Thr Ile Ser Leu Ile Gln Gln Lys Leu Ser
 123 370 375 380
 126 Val Phe Gln Glu Met Phe Glu Thr Phe Thr Glu Ser Arg Ile Val
 127 385 390 395 400
 130 Glu Trp Thr Lys Lys Ile Gln Asp Ile Val Arg Arg Arg Gln Leu Leu
 131 405 410 415
 134 Thr Val Phe Arg Glu Gly Lys Asp Gly Gln Gln Asp Val Asp Val Ala
 135 420 425 430
 138 Ile Leu Gln Ala Leu Leu Lys Ala Ser Arg Ser Gln Asp His Phe Gly
 139 435 440 445
 142 His Glu Asn Trp Asp His Gln Leu Lys Leu Ala Val Ala Trp Asn Arg
 143 450 455 460
 146 Val Asp Ile Ala Arg Ser Glu Ile Phe Met Asp Glu Trp Gln Trp Lys
 147 465 470 475 480
 150 Pro Ser Asp Leu His Pro Thr Met Thr Ala Ala Leu Ile Ser Asn Lys
 151 485 490 495
 154 Pro Glu Phe Val Lys Leu Phe Leu Glu Asn Gly Val Gln Leu Lys Glu
 155 500 505 510
 158 Phe Val Thr Trp Asp Thr Leu Leu Tyr Leu Tyr Glu Asn Leu Asp Pro
 159 515 520 525
 162 Ser Cys Leu Phe His Ser Lys Leu Gln Lys Val Leu Val Glu Asp Pro
 163 530 535 540
 166 Glu Arg Pro Ala Cys Ala Pro Ala Ala Pro Arg Leu Gln Met His His
 167 545 550 555 560
 170 Val Ala Gln Val Leu Arg Glu Leu Leu Gly Asp Phe Thr Gln Pro Leu
 171 565 570 575
 174 Tyr Pro Arg Pro Arg His Asn Asp Arg Leu Arg Leu Leu Leu Pro Val
 175 580 585 590
 178 Pro His Val Lys Leu Asn Val Gln Gly Val Ser Leu Arg Ser Leu Tyr

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179	595	600	605	
182	Lys Arg Ser Ser Gly His Val Thr Phe Thr Met Asp Pro Ile Arg Asp			
183	610	615	620	
186	Leu Leu Ile Trp Ala Ile Val Gln Asn Arg Arg Glu Leu Ala Gly Ile			
187	625	630	635	640
190	Ile Trp Ala Gln Ser Gln Asp Cys Ile Ala Ala Ala Leu Ala Cys Ser			
191	645	650	655	
194	Lys Ile Leu Lys Glu Leu Ser Lys Glu Glu Glu Asp Thr Asp Ser Ser			
195	660	665	670	
198	Glu Glu Met Leu Ala Leu Ala Glu Glu Tyr Glu His Arg Ala Ile Gly			
199	675	680	685	
202	Val Phe Thr Glu Cys Tyr Arg Lys Asp Glu Glu Arg Ala Gln Lys Leu			
203	690	695	700	
206	Leu Thr Arg Val Ser Glu Ala Trp Gly Lys Thr Thr Cys Leu Gln Leu			
207	705	710	715	720
210	Ala Leu Glu Ala Lys Asp Met Lys Phe Val Ser His Gly Gly Ile Gln			
211	725	730	735	
214	Ala Phe Leu Thr Lys Val Trp Trp Gly Gln Leu Ser Val Asp Asn Gly			
215	740	745	750	
218	Leu Trp Arg Val Thr Leu Cys Met Leu Ala Phe Pro Leu Leu Leu Thr			
219	755	760	765	
222	Gly Leu Ile Ser Phe Arg Glu Lys Arg Leu Gln Asp Val Gly Thr Pro			
223	770	775	780	
226	Ala Ala Arg Ala Arg Ala Phe Phe Thr Ala Pro Val Val Val Phe His			
227	785	790	795	800
230	Leu Asn Ile Leu Ser Tyr Phe Ala Phe Leu Cys Leu Phe Ala Tyr Val			
231	805	810	815	
234	Leu Met Val Asp Phe Gln Pro Val Pro Ser Trp Cys Glu Cys Ala Ile			
235	820	825	830	
238	Tyr Leu Trp Leu Phe Ser Leu Val Cys Glu Glu Met Arg Gln Leu Phe			
239	835	840	845	
242	Tyr Asp Pro Asp Glu Cys Gly Leu Met Lys Lys Ala Ala Leu Tyr Phe			
243	850	855	860	
246	Ser Asp Phe Trp Asn Lys Leu Asp Val Gly Ala Ile Leu Leu Phe Val			
247	865	870	875	880
250	Ala Gly Leu Thr Cys Arg Leu Ile Pro Ala Thr Leu Tyr Pro Gly Arg			
251	885	890	895	
254	Val Ile Leu Ser Leu Asp Phe Ile Leu Phe Cys Leu Arg Leu Met His			
255	900	905	910	
258	Ile Phe Thr Ile Ser Lys Thr Leu Gly Pro Lys Ile Ile Ile Val Lys			
259	915	920	925	
262	Arg Met Met Lys Asp Val Phe Phe Leu Phe Leu Leu Ala Val Trp			
263	930	935	940	
266	Val Val Ser Phe Gly Val Ala Lys Gln Ala Ile Leu Ile His Asn Glu			
267	945	950	955	960
270	Arg Arg Val Asp Trp Leu Phe Arg Gly Ala Val Tyr His Ser Tyr Leu			
271	965	970	975	
274	Thr Ile Phe Gly Gln Ile Pro Gly Tyr Ile Asp Gly Val Asn Phe Asn			
275	980	985	990	

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278 Pro Glu His Cys Ser Pro Asn Gly Thr Asp Pro Tyr Lys Pro Lys Cys
279 995 1000 1005
282 Pro Glu Ser Asp Ala Thr Gln Gln Arg Pro Ala Phe Pro Glu Trp
283 1010 1015 1020
286 Leu Thr Val Leu Leu Leu Cys Leu Tyr Leu Leu Phe Thr Asn Ile
287 1025 1030 1035
290 Leu Leu Leu Asn Leu Leu Ile Ala Met Phe Asn Tyr Thr Phe Gln
291 1040 1045 1050
294 Gln Val Gln Glu His Thr Asp Gln Ile Trp Lys Phe Gln Arg His
295 1055 1060 1065
298 Asp Leu Ile Glu Glu Tyr His Gly Arg Pro Ala Ala Pro Pro Pro
299 1070 1075 1080
302 Phe Ile Leu Leu Ser His Leu Gln Leu Phe Ile Lys Arg Val Val
303 1085 1090 1095
306 Leu Lys Thr Pro Ala Lys Arg His Lys Gln Leu Lys Asn Lys Leu
307 1100 1105 1110
310 Glu Lys Asn Glu Glu Ala Ala Leu Leu Ser Trp Glu Ile Tyr Leu
311 1115 1120 1125
314 Lys Glu Asn Tyr Leu Gln Asn Arg Gln Phe Gln Gln Lys Gln Arg
315 1130 1135 1140
318 Pro Glu Gln Lys Ile Glu Asp Ile Ser Asn Lys Val Asp Ala Met
319 1145 1150 1155
322 Val Asp Leu Leu Asp Leu Asp Pro Leu Lys Arg Ser Gly Ser Met
323 1160 1165 1170
326 Glu Gln Arg Leu Ala Ser Leu Glu Glu Gln Val Ala Gln Thr Ala
327 1175 1180 1185
330 Arg Ala Leu His Trp Ile Val Arg Thr Leu Arg Ala Ser Gly Phe
331 1190 1195 1200
334 Ser Ser Glu Ala Asp Val Pro Thr Leu Ala Ser Gln Lys Ala Ala
335 1205 1210 1215
338 Glu Glu Pro Asp Ala Glu Pro Gly Gly Arg Lys Lys Thr Glu Glu
339 1220 1225 1230
342 Pro Gly Asp Ser Tyr His Val Asn Ala Arg His Leu Leu Tyr Pro
343 1235 1240 1245
346 Asn Cys Pro Val Thr Arg Phe Pro Val Pro Asn Glu Lys Val Pro
347 1250 1255 1260
350 Trp Glu Thr Glu Phe Leu Ile Tyr Asp Pro Pro Phe Tyr Thr Ala
351 1265 1270 1275
354 Glu Arg Lys Asp Ala Ala Ala Met Asp Pro Met Gly Asp Thr Leu
355 1280 1285 1290
358 Glu Pro Leu Ser Thr Ile Gln Tyr Asn Val Val Asp Gly Leu Arg
359 1295 1300 1305
362 Asp Arg Arg Ser Phe His Gly Pro Tyr Thr Val Gln Ala Gly Leu
363 1310 1315 1320
366 Pro Leu Asn Pro Met Gly Arg Thr Gly Leu Arg Gly Arg Gly Ser
367 1325 1330 1335
370 Leu Ser Cys Phe Gly Pro Asn His Thr Leu Tyr Pro Met Val Thr
371 1340 1345 1350
374 Arg Trp Arg Arg Asn Glu Asp Gly Ala Ile Cys Arg Lys Ser Ile

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375	1355	1360	1365												
378	Lys	Met	Leu	Glu	Val	Leu	Val	Val	Lys	Leu	Pro	Leu	Ser	Glu	
379	1370	1375	1380												
382	His	Trp	Ala	Leu	Pro	Gly	Gly	Ser	Arg	Glu	Pro	Gly	Glu	Met	Leu
383	1385	1390	1395												
386	Pro	Arg	Lys	Leu	Lys	Arg	Ile	Leu	Arg	Gln	Glu	His	Trp	Pro	Ser
387	1400	1405	1410												
390	Phe	Glu	Asn	Leu	Leu	Lys	Cys	Gly	Met	Glu	Val	Tyr	Lys	Gly	Tyr
391	1415	1420	1425												
394	Met	Asp	Asp	Pro	Arg	Asn	Thr	Asp	Asn	Ala	Trp	Ile	Glu	Thr	Val
395	1430	1435	1440												
398	Ala	Val	Ser	Val	His	Phe	Gln	Asp	Gln	Asn	Asp	Val	Glu	Leu	Asn
399	1445	1450	1455												
402	Arg	Leu	Asn	Ser	Asn	Leu	His	Ala	Cys	Asp	Ser	Gly	Ala	Ser	Ile
403	1460	1465	1470												
406	Arg	Trp	Gln	Val	Val	Asp	Arg	Arg	Ile	Pro	Leu	Tyr	Ala	Asn	His
407	1475	1480	1485												
410	Lys	Thr	Leu	Leu	Gln	Lys	Ala	Ala	Ala	Glu	Phe	Gly	Ala	His	Tyr
411	1490	1495	1500												

414 <210> SEQ ID NO: 2

415 <211> LENGTH: 4512

416 <212> TYPE: DNA

417 <213> ORGANISM: Homo sapiens

419 <400> SEQUENCE: 2

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422	cccagaaggg	tcactgacct	ggggatggc	tccaatctcc	ggcgcagcaa	cagcagccctc	120
424	ttcaagagct	ggaggctaca	gtgcccctc	ggcaacaatg	acaagcaaga	aagcctcagt	180
426	tctggattc	ctgaaaacat	caagaagaaa	gaatcgctgt	attttgcgtt	aagttccaaa	240
428	ctgtctgtat	ctggaaaggt	ggtgtgtcag	tgtgcgtaca	cgcgtcgac	gcacttggag	300
430	gaggctacca	agccccacac	cttccagggc	acacagtggg	acccaaagaa	acatgtccag	360
432	gagatgccaa	ccgatgcctt	tggcgacatc	gtcttcacgg	gcctgagcca	gaaggtgaaa	420
434	aagtacgtcc	gagtctccca	ggacacgccc	tccagcgtga	tctaccaccc	catgaccagg	480
436	cactggggc	tggacgtccc	caatctctt	atctcggtga	ccgggggggc	caagaacttc	540
438	aacatgaagc	cgcggctgaa	gagcattttc	cgcagaggcc	tggtcaaggt	ggctcagacc	600
440	acagggggct	ggatcatcac	aggggggtcc	cacaccggcg	tcatgaagca	ggtaggcgag	660
442	gcgggtcgccc	acttcagcct	gagcagcagc	tacaaggaag	gcgagctcat	caccatcgga	720
444	gtcgcacact	ggggcactgt	ccaccggcc	gaggcctga	tccatccac	gggcagcttc	780
446	ccgcggaggt	acatacttgg	tgaggatggc	caagggaaacc	tgacctgcct	agacagcaac	840
448	cactctca	tcatccctcg	ggacgacggg	acccacggcc	agtacgggg	ggagattcct	900
450	ctgaggacca	ggctggagaa	gttcatatcg	gagcagacca	aggaaagagg	aggtgtggcc	960
452	atcaagatcc	ccatcggtgt	cgtggtgcgt	gagggcggcc	cgggcacgtt	gcacaccatc	1020
454	gacaacgcca	ccaccaacgg	cacccctgt	gtgggtgtgg	agggctcggt	ccgcgtggcc	1080
456	gacgtcatgt	cccagggtggc	caacctgcct	gtctcgacaa	tcaatatctc	cctgatccag	1140
458	cagaaactga	gcgtgttctt	ccaggagatg	tttgagaccc	tcacggaaag	caggattgtc	1200
460	gagtggacca	aaaagatcca	agatattgtc	cggaggcggc	agctgtgtac	tgtcttccgg	1260
462	gaaggcaagg	atggtcagca	ggacgtggat	gtggccatct	tgcaggcctt	gctgaaagcc	1320
464	tcacggagcc	aagaccactt	tggccacagag	aactgggacc	accagctgaa	actggcagtg	1380
466	gcatggaatc	gcgtggacat	tgcccgcgt	gagatctca	tggatgagtg	gcagtggaaag	1440
468	cttcagatc	tgcacccac	gatgacagct	gcactcatct	ccaacaagcc	tgagttgtg	1500

VERIFICATION SUMMARY

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Input Set : A:\A70040-1.ST25.txt

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